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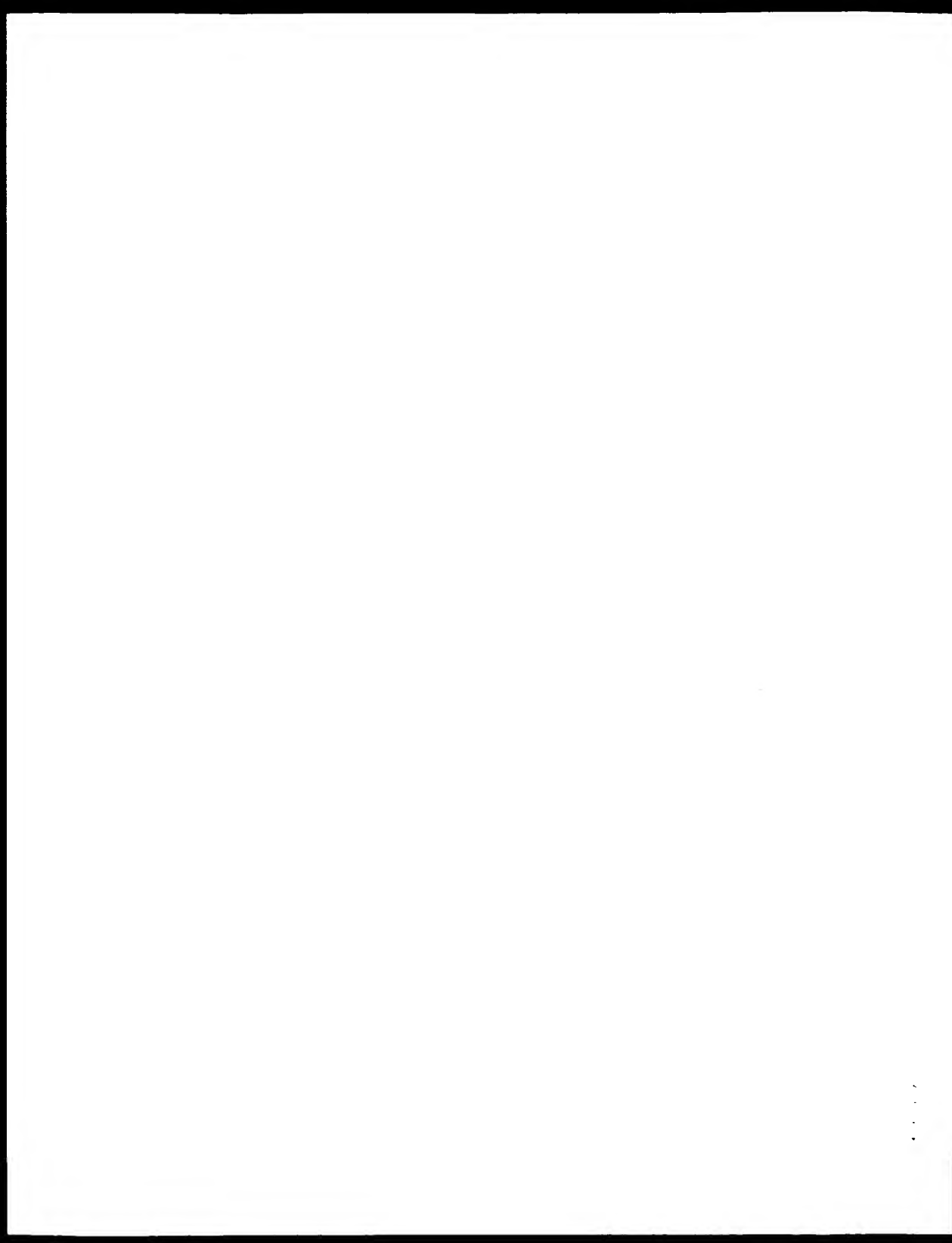
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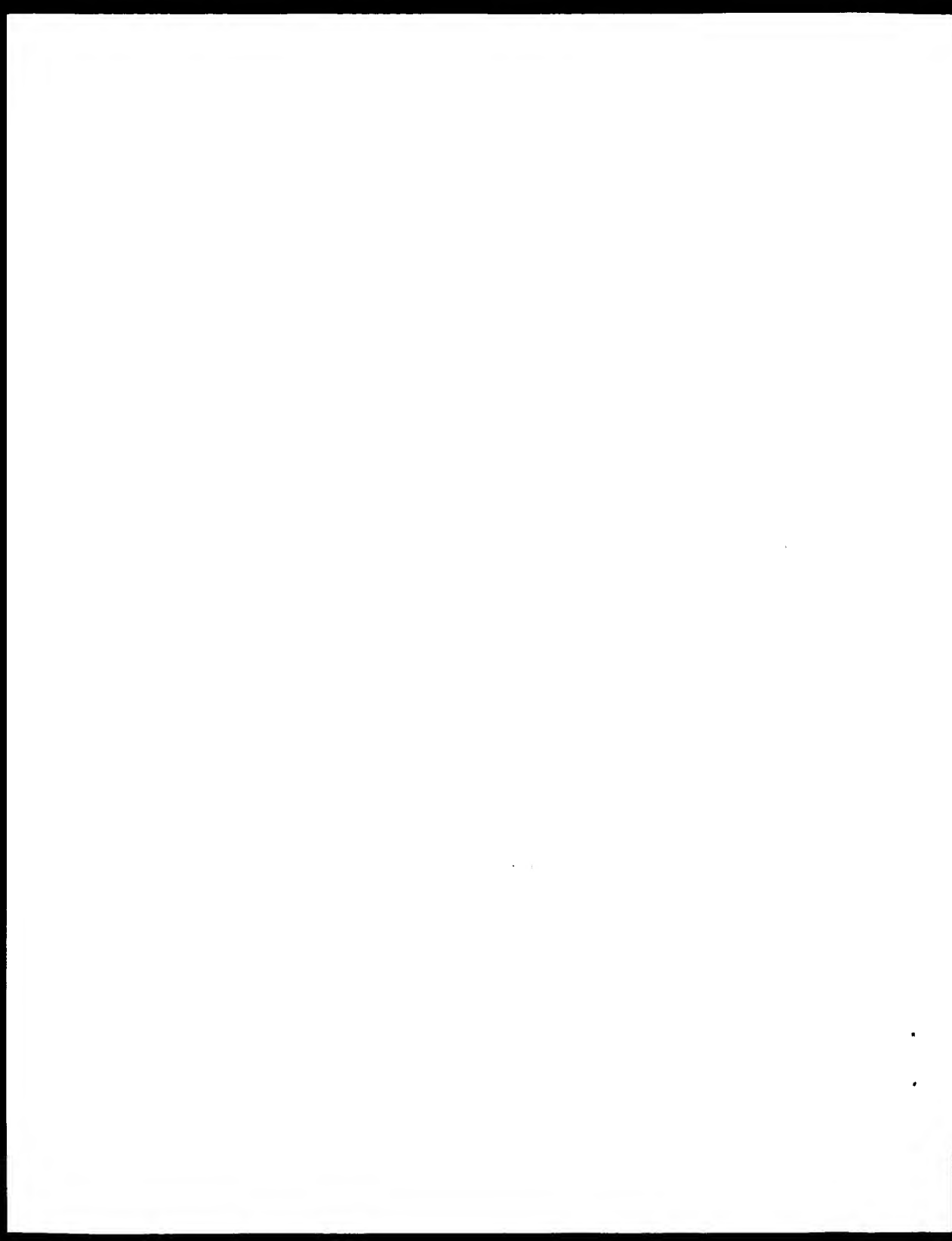

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1 TITLE OF INVENTION: MITIGIOUS AND COMPOSITIONS FOR THE
2
3 TITLE OF INVENTION: DIAGNOSTIC AND TREATMENT OF CATARACTS
4
5 NUMBER OF SEQUENCES: 33
6
7 CORRESPONDENT'S ADDRESS:
8
9 ADDRESSEE: FURRY, ROAG & ELIOT LLP
10 STREET: One Post Office Square
11 CITY: Boston
12 STATE: MA
13 COUNTRY: USA
14 PUBLICATION NO.: 20170
15 COMPUTER READABLE FORM:
16
17 MICROFILM FILE: floppy disk
18 COMPUTER: IBM PC compatible
19
20 SOFTWARE: Patent In Review #1,205
21
22 CURRENT APPLICATION DATA:
23
24 A.I. # 1: 1,200-6 5, 20, 257, 151
25
26 FILING DATE: 24-OCT-1997
27
28 CLASSIFICATION: 435
29
30 NAME OF AGENT/REGISTRATION:
31
32 REGISTRATION NUMBER: 35,430
33
34 SERIALS: 1,200-6 5, 20, 257, 151 A, 924-01
35
36 TELECOMMUNICATION INFORMATION:
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38 TELEPHONE: 617-432-1000
39
40 FAX: 617-432-7009
41
42 INFORMATION FOR SEQ ID NO: 5:
43
44 SEQUENCE CHARACTERISTICS:
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46 LENGTH: 1017 base pairs
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48 TYPE: nucleic acid
49
50 STRATEGY: standard
51
52 TOPOLOGY: linear
53
54 MOLECULE TYPE: cDNA
55
56 US-08-957-151-5
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58 Query Match 9.8% Score 56.4; DB 4; Length: 1017
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60 Best Local Similarity 52.9% Prod. No. 2,1e-052
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62 Mismatch 18% Mismatch Pos 176

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1 APPLICANT: 2
3 TIME OF INVENTION: NOVEL METHOD FOR TESTING THE
4 TITLE OF INVENTION: DIFFERENTIATION STATUS IN PATENTS: 11/11/1988
5 NUMBER OF SEQUENCES: 16
6 COMPUTER READABLE FORM:
7 MEDIUM TYPE: Floppy disk
8 CUMULATIVE: IBM PC compatible

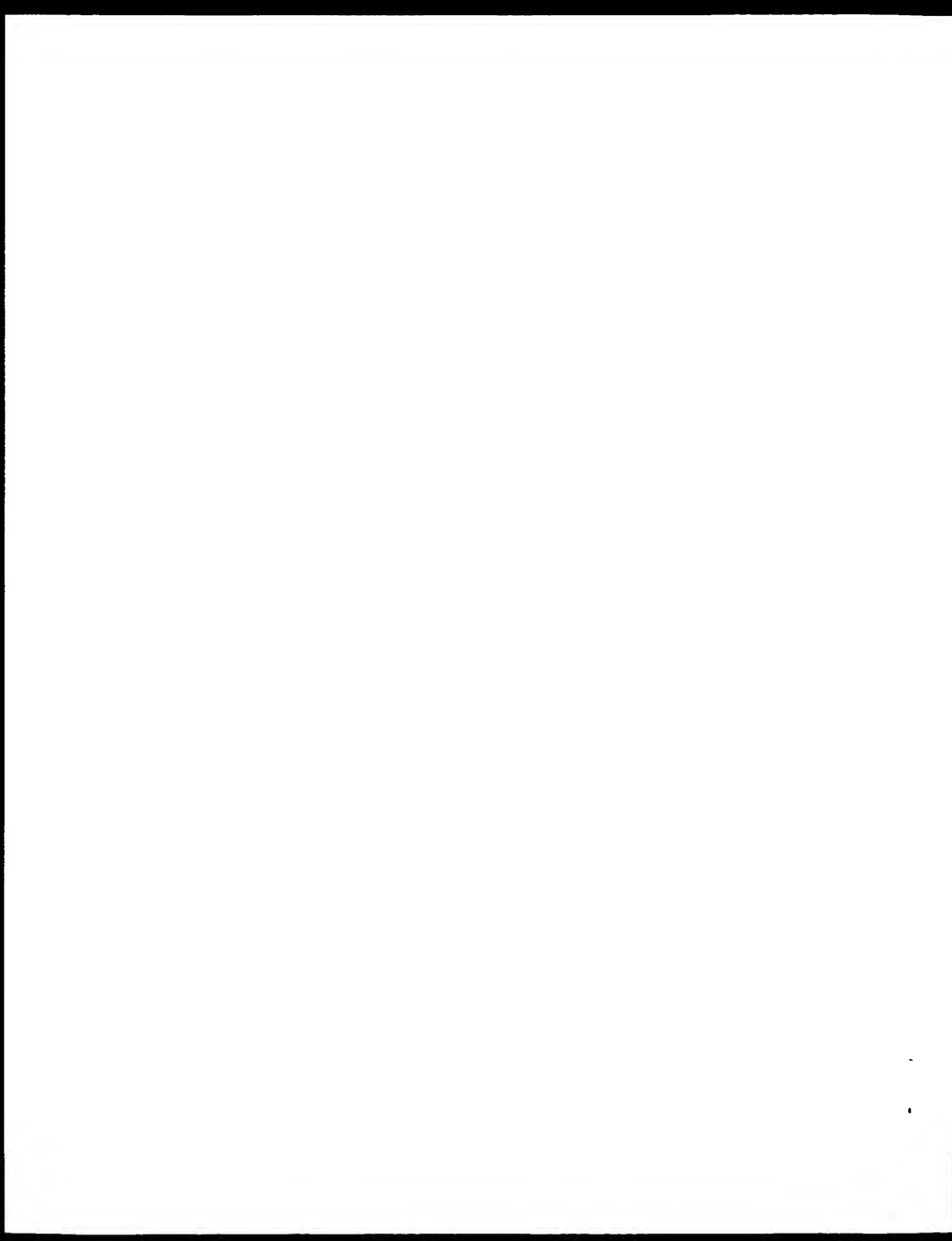


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of 1257096-1258641, 1460064-1470989, and 1476592-1476743.
SUBMITTABLE BY genome sources and M. Patrick Holland.
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ORGANISM Homo sapiens Pigeonpea, *Cajanus cajan* Entolobosoma

REFERENCE
1. Classes 1 to 433
Mammalia; Embryos; Primates; Carnivores; Homiidae; Homo.
Mammalia; Embryos; Primates; Carnivores; Homiidae; Homo.

TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP).

JOURNAL OF
THEORY AND PRACTICE
OF THE
TEACHING OF
ENGLISH AS A
SECOND LANGUAGE
Volume 19 Number 1
Spring 1997

NEUMANN, J. 1990. *Neurobiology of the Human Brain*. New York: Plenum Press.

Yuryo Petrovich; Christofor A. Moskaluk, M.D., Ph.D.; Michael K. Parnotzky, M.D., Ph.D.

RNA Library Preparation: M. Bento Soares, Ph.D., M. F. Almeida, Ph.D., Remédios, Ph.D.

RNA Library Arrayed by: Greg Lomon, Ph.D.
Cell Compaction by: Michael A. Delaney, Systems Engineering Center

average distribution; NPL CWP change distribution information can be found through the L.M.A. Web page: <http://lma.dti.gov>.

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Seq primer: 40bp from Gdco,
Location/Qualifiers

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4th - 8th, n = 380; 96.06%,
/c100000 IMAGE: 2241297 =

Volume—The "New York Times"
Issue—Type of material deemed controversial

$$\begin{aligned} & \text{f_db_test} = \text{fit(} \theta \text{)} \\ & \text{f_test} = \text{predict(} \text{f_db_test}, \text{X_test) } \end{aligned}$$

from the normalized library N1 (Table 3) was prepared, and sequenced, and the results are shown in Table 4.

This tRNA was used as primer in a solid-phase hybridization experiment, followed by the subsequent labeling of the cDNA fragments in vitro.

of 5,000 colonies made from the same library (clonings) revealed that the driver was responsible for 60% of all clones.

[illegible]

REGIN

Quality Match

Match	Conserved	Mismatches	Indels	Gaps
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[illegible]
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[illegible][illegible][illegible][illegible]

219 220 221 222 223 224 225 226 227 228 229 230 231 232 233 234 235 236 237 238 239 240 241 242 243 244 245 246 247 248 249 250 251 252 253 254 255 256 257 258 259 260 261 262 263 264 265 266 267 268 269 270 271 272 273 274 275 276 277 278 279 280 281 282 283 284 285 286 287 288 289 290 291 292 293 294 295 296 297 298 299 300 301 302 303 304 305 306 307 308 309 310 311 312 313 314 315 316 317 318 319 320 321 322 323 324 325 326 327 328 329 330 331 332 333 334 335 336 337 338 339 340 341 342 343 344 345 346 347 348 349 350 351 352 353 354 355 356 357 358 359 360 361 362 363 364 365 366 367 368 369 370 371 372 373 374 375 376 377 378 379 380 381 382 383 384 385 386 387 388 389 390 391 392 393 394 395 396 397 398 399 400 401 402 403 404 405 406 407 408 409 410 411 412 413 414 415 416 417 418 419 420 421 422 423 424 425 426 427 428 429 430 431 432 433 434 435 436 437 438 439 440 441 442 443 444 445 446 447 448 449 450 451 452 453 454 455 456 457 458 459 460 461 462 463 464 465 466 467 468 469 470 471 472 473 474 475 476 477 478 479 480 481 482 483 484 485 486 487 488 489 490 491 492 493 494 495 496 497 498 499 500 501 502 503 504 505 506 507 508 509 510 511 512 513 514 515 516 517 518 519 520 521 522 523 524 525 526 527 528 529 530 531 532 533 534 535 536 537 538 539 540 541 542 543 544 545 546 547 548 549 550 551 552 553 554 555 556 557 558 559 560 561 562 563 564 565 566 567 568 569 570 571 572 573 574 575 576 577 578 579 580 581 582 583 584 585 586 587 588 589 590 591 592 593 594 595 596 597 598 599 600 601 602 603 604 605 606 607 608 609 610 611 612 613 614 615 616 617 618 619 620 621 622 623 624 625 626 627 628 629 630 631 632 633 634 635 636 637 638 639 640 641 642 643 644 645 646 647 648 649 650 651 652 653 654 655 656 657 658 659 660 661 662 663 664 665 666 667 668 669 670 671 672 673 674 675 676 677 678 679 680 681 682 683 684 685 686 687 688 689 690 691 692 693 694 695 696 697 698 699 700 701 702 703 704 705 706 707 708 709 710 711 712 713 714 715 716 717 718 719 720 721 722 723 724 725 726 727 728 729 730 731 732 733 734 735 736 737 738 739 740 741 742 743 744 745 746 747 748 749 750 751 752 753 754 755 756 757 758 759 760 761 762 763 764 765 766 767 768 769 770 771 772 773 774 775 776 777 778 779 780 781 782 783 784 785 786 787 788 789 790 791 792 793 794 795 796 797 798 799 800 801 802 803 804 805 806 807 808 809 810 811 812 813 814 815 816 817 818 819 820 821 822 823 824 825 826 827 828 829 830 831 832 833 834 835 836 837 838 839 840 841 842 843 844 845 846 847 848 849 850 851 852 853 854 855 856 857 858 859 860 861 862 863 864 865 866 867 868 869 870 871 872 873 874 875 876 877 878 879 880 881 882 883 884 885 886 887 888 889 890 891 892 893 894 895 896 897 898 899 900 901 902 903 904 905 906 907 908 909 910 911 912 913 914 915 916 917 918 919 920 921 922 923 924 925 926 927 928 929 930 931 932 933 934 935 936 937 938 939 940 941 942 943 944 945 946 947 948 949 950 951 952 953 954 955 956 957 958 959 960 961 962 963 964 965 966 967 968 969 970 971 972 973 974 975 976 977 978 979 980 981 982 983 984 985 986 987 988 989 990 991 992 993 994 995 996 997 998 999 1000 1001 1002 1003 1004 1005 1006 1007 1008 1009 1010 1011 1012 1013 1014 1015 1016 1017 1018 1019 1020 1021 1022 1023 1024 1025 1026 1027 1028 1029 1030 1031 1032 1033 1034 1035 1036 1037 1038 1039 1040 1041 1042 1043 1044 1045 1046 1047 1048 1049 1050 1051 1052 1053 1054 1055 1056 1057 1058 1059 1060 1061 1062 1063 1064 1065 1066 1067 1068 1069 1070 1071 1072 1073 1074 1075 1076 1077 1078 1079 1080 1081 1082 1083 1084 1085 1086 1087 1088 1089 1090 1091 1092 1093 1094 1095 1096 1097 1098 1099 1100 1101 1102 1103 1104 1105 1106 1107 1108 1109 1110 1111 1112 1113 1114 1115 1116 1117 1118 1119 1120 1121 1122 1123 1124 1125 1126 1127 1128 1129 1130 1131 1132 1133 1134 1135 1136 1137 1138 1139 1140 1141 1142 1143 1144 1145 1146 1147 1148 1149 1150 1151 1152 1153 1154 1155 1156 1157 1158 1159 1160 1161 1162 1163 1164 1165 1166 1167 1168 1169 1170 1171 1172 1173 1174 1175 1176 1177 1178 1179 1180 1181 1182 1183 1184 1185 1186 1187 1188 1189 1190 1191 1192 1193

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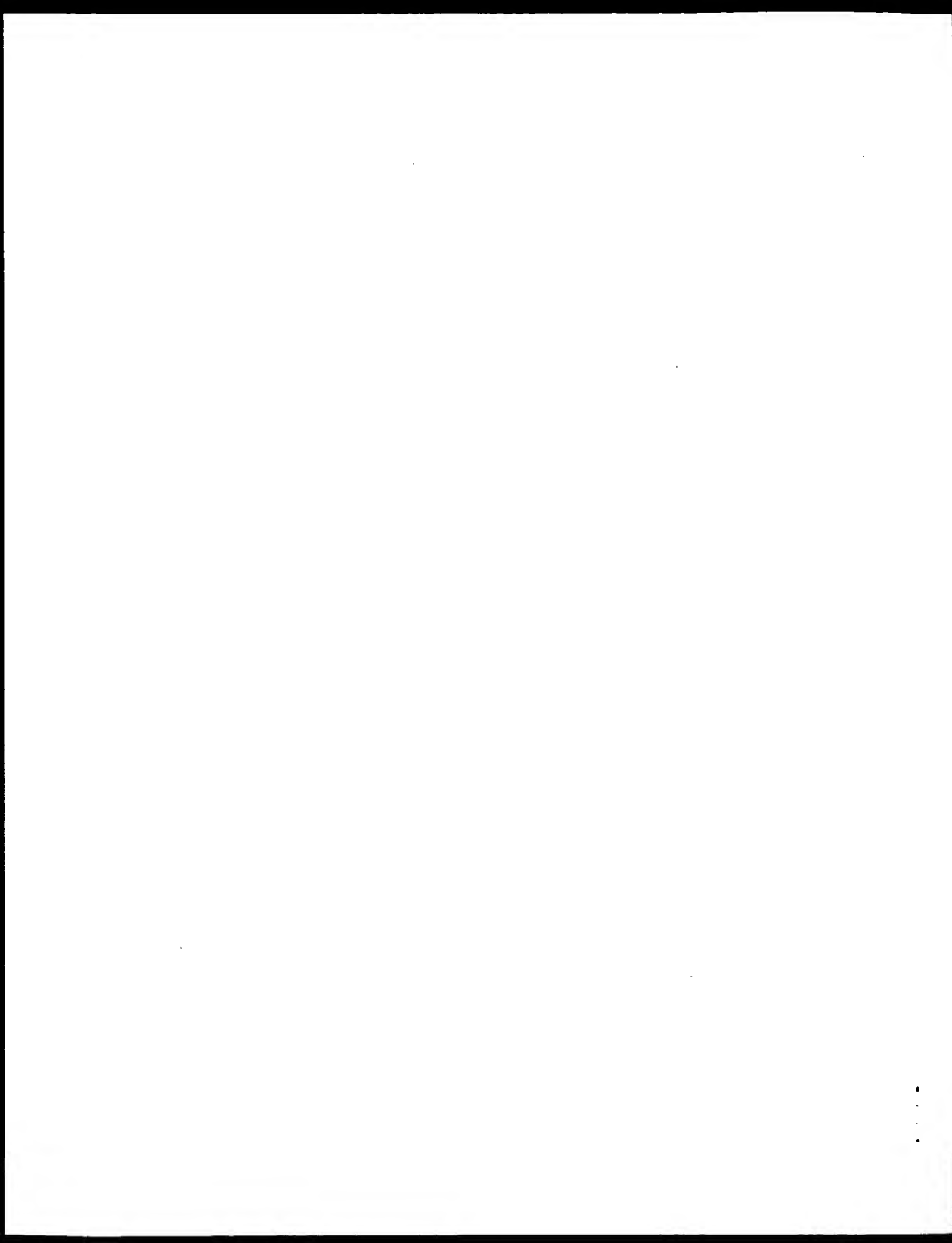
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RESULT 4
US (H 957-451-0)
: SUBJECT: Application; US/0007451
: Patent No. 6,06566
: GENERAL INFORMATION:
: APPLICANT: Semtech, Inc.
: APPLICANT: Mottley, Jeffrey R.

[illegible]

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COUNTRY: USA
ZIP: 02109-2170
COMPUTER HEADLINE FORM:
MESSAGE TYPE: floppy disk
COMPUTER: IBM PC compatible
SUBJECT: SYSTEM: F-15; 2005
SOFTWARE: Patent in Release #1.0
Version: 1.1.0

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[illegible]

[illegible]

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RESULT 9
US 09 606 75A 2
; Sequence 2, Application US/096 067 5A
; Patent No. 641656
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; GENERAL INFORMATION:
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; TITLE OF INVENTION: 641656/Transcription Factor, p11
; CLASS. NO.: 27.4, C12:000
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; CURRENT APPLICATION NUMBER: 05297646, 75A
; FILING DATE: 2000 08 11
; NUMBER OF SEQ. IDS: 25
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; SOFTWARE: Patent Invention 3.0
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; SEQ. ID NO.: 240

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1	NAME: NAME	16. 58	Score: 161	OR 4:	Length: 243
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3	NAME: NAME	45	Conservative	40	Mismatches
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77	NAME: NAME				

RESULT 10
05/07/66-7/06/67
PATENT NO. 6416956
PATENT NO. 6416956
GENERAL INFORMATION:
APPLICANT: BERD, PATRICIA
TITLE OF INVENTION: NO. 6416956el Transposition Factor, 5el1
FILE REFERENCE: 179, 474,05X00
CURRENT APPLICATION NUMBER: US/009/6, 06, 7 6A
PENDING FILING DATE: 2000-08-11
NUMBER OF SEQ ID NOS: 25
SOFTWARE: PATENT IN VERSION 4.0
SEQUENCE ID:
TYPE: PAT
ORIGIN: B.M. sapiens
FEATURE:
NAME/KEY: BELX 1


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10 184 GPTQGGGQGGGAGGENTSSSSG-----EISEAQMREIQR 222
QY 100 NNDQTRTKETLQVTELESVPHIYVTHVTRPELAINGVTRKVAQWVKKRPAQR 179
10 223 KIQ--KRRSTGPAVLPFRFTTWTHTVTHVTRKVAQWVKKRPAQR 200
QY 160 RHQELMLANELR 172
10 281 REEK--LRNQRR 290

RESULT 14
US 08 778-304 2
: Sequence 2, Application US/0878404
: Patent No. 6028184
: GENERAL INFORMATION:
: APPLICANT:
: TITLE OF INVENTION: NOVEL METHOD FOR TESTING THE
: NUMBER OF SEQUENCES: 4
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: SOFTWARE: Patcom 10 Release #1.0, Version #1.30 (EPO)
: CURRENT APPLICATION DATA: us/09/778, 304
: APPLICATION NUMBER: us/09/778, 304
: FILING DATE:
: CLASSIFICATION: 514
: INFORMATION FOR SEQ ID NO: 2:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 179 amino acids
: TYPE: amino acid
: TOPOLOGY: Linear
: MOLECULE TYPE: protein
US 08 778-304-2

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Best Local Similarity 40 8%; Prod. No. 4,70 0%;
Matches 41; Consistency 38; Mismatches 46; Indels 26; Gaps 0
QY 40 GAVTGMNNPQGVNHRGNNRSGQMDRSGGNGRSGGQGPPTPEPAQAEKRGTF 90
10 111 111 111 111 111 111 111 111 111 111 111 111 111
10 184 GPTQGGGQGGGAGGENTSSSSG-----EISEAQMREIQR 222
QY 100 NNDQTRTKETLQVTELESVPHIYVTHVTRPELAINGVTRKVAQWVKKRPAQR 179
10 223 KIQ--KRRSTGPAVLPFRFTTWTHTVTHVTRKVAQWVKKRPAQR 200
QY 160 RHQELMLANELR 172
10 281 REEK--LRNQRR 290

RESULT 15
US 08 778-424 4
: Sequence 4, Application US/0878424
: Patent No. 6021697
: GENERAL INFORMATION:
: APPLICANT:
: TITLE OF INVENTION: NOVEL METHOD FOR TESTING THE
: NUMBER OF SEQUENCES: 6
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: SOFTWARE: Patcom 10 Release #1.0, Version #1.40 (EPO)
: CURRENT APPLICATION DATA: us/09/778, 424
: APPLICATION NUMBER: us/09/778, 424

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: FILING DATE: December 31, 1996
: INFORMATION:
: SEQUENCE CHARACTERISTICS: 4
: LENGTH: 440 amino acids
: TYPE: amino acid
: TOPOLOGY: Linear
: MOLECULE TYPE: protein
US 08 778-424 4
Query Match 16 0% Score 156 40 4; Length 4 4;
Best Local Similarity 40 8%; Prod. No. 4,70 0%;
Matches 41; Consistency 38; Mismatches 46; Indels 26; Gaps 0
QY 40 GAVTGMNNPQGVNHRGNNRSGQMDRSGGNGRSGGQGPPTPEPAQAEKRGTF 90
10 111 111 111 111 111 111 111 111 111 111 111 111 111
10 184 GPTQGGGQGGGAGGENTSSSSG-----EISEAQMREIQR 222
QY 100 NNDQTRTKETLQVTELESVPHIYVTHVTRPELAINGVTRKVAQWVKKRPAQR 179
10 223 KIQ--KRRSTGPAVLPFRFTTWTHTVTHVTRKVAQWVKKRPAQR 200
QY 160 RHQELMLANELR 172
10 281 REEK--LRNQRR 290
Search completed: Apr 11 28, 2003, 04:05:27
Job Clnr: 33 seqs

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GenCore version 5.1.4.05.4578
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OM protein - protein search, using sw model

Run on: April 29, 2003, 13:55:57, Search time: 007 seconds
802176 hits (0.001464672)

Title: US-09-867-753-2

Perfect score: 986

Sequence: 1 MARSLVHIVYGLSVQVQV.....IM-ANGELADPECVIVVD 184

Scoring table: R05M92

Gap: 10.0, Gapex: 0.5

Searched: 101932 seqs, 80129403 residues

Total number of hits satisfying chosen parameters: 20752

Minimum DB seq length: 0

Maximum hit seq length: 25000000

Post-processing: Minimum Match: 0%

Maximum Match: 100%

Listing first 45 summaries

Database:

1: Published Applications AA*
2: ...
3: ...
4: ...
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14: ...

pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being plotted, and is derived by analysis of the total score distribution.

SUMMARIES

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1	986	100.0	184	0	US-09-867-753-2
2	985	100.0	184	0	US-09-867-753-2
3	984	99.9	184	0	US-09-867-753-2
4	983	99.8	184	0	US-09-867-753-2
5	982	99.7	184	0	US-09-867-753-2
6	981	99.6	184	0	US-09-867-753-2
7	980	99.5	184	0	US-09-867-753-2
8	979	99.4	184	0	US-09-867-753-2
9	978	99.3	184	0	US-09-867-753-2
10	977	99.2	184	0	US-09-867-753-2
11	976	99.1	184	0	US-09-867-753-2
12	975	99.0	184	0	US-09-867-753-2
13	974	98.9	184	0	US-09-867-753-2
14	973	98.8	184	0	US-09-867-753-2
15	972	98.7	184	0	US-09-867-753-2
16	971	98.6	184	0	US-09-867-753-2
17	970	98.5	184	0	US-09-867-753-2
18	969	98.4	184	0	US-09-867-753-2
19	968	98.3	184	0	US-09-867-753-2

20	144.5	14.7	324	10	US-09-749-7389-9	Sequence 9, Appl 1
21	144.5	14.7	324	10	US-09-900-5279-9	Sequence 9, Appl 1
22	141.5	14.4	351	10	US-09-759-847-5	Sequence 1, Appl 1
23	140	14.2	147	9	US-09-222-880-136	Sequence 336, App
24	140	14.2	147	9	US-09-222-880-136	Sequence 336, App
25	140	14.2	147	9	US-09-952-751-335	Sequence 336, App
26	140	14.2	147	9	US-09-895-814-376	Sequence 336, App
27	140	14.2	147	10	US-09-259-143-336	Sequence 336, App
28	140	14.2	147	10	US-09-259-143-336	Sequence 336, App
29	140	14.2	147	10	US-09-895-814-376	Sequence 336, App
30	140	14.2	147	10	US-09-895-814-376	Sequence 336, App
31	140	14.2	147	10	US-09-895-814-376	Sequence 336, App
32	140	14.2	147	10	US-09-895-814-376	Sequence 336, App
33	140	14.2	147	10	US-09-895-814-376	Sequence 336, App
34	140	14.2	147	10	US-09-895-814-376	Sequence 336, App
35	140	14.2	147	10	US-09-895-814-376	Sequence 336, App
36	140	14.2	147	10	US-09-895-814-376	Sequence 336, App
37	140	14.2	147	10	US-09-895-814-376	Sequence 336, App
38	140	14.2	147	10	US-09-895-814-376	Sequence 336, App
39	140	14.2	147	10	US-09-895-814-376	Sequence 336, App
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41	140	14.2	147	10	US-09-895-814-376	Sequence 336, App
42	140	14.2	147	10	US-09-895-814-376	Sequence 336, App
43	140	14.2	147	10	US-09-895-814-376	Sequence 336, App
44	140	14.2	147	10	US-09-895-814-376	Sequence 336, App
45	140	14.2	147	10	US-09-895-814-376	Sequence 336, App

ALIGNMENTS

ALIGNMENT 1
Query: 1 MARSLVHIVYGLSVQVQV.....IM-ANGELADPECVIVVD 184
Subject: 1 MARSLVHIVYGLSVQVQV.....IM-ANGELADPECVIVVD 184
Score: 986, Ident: 100.0, Pos: 184, Neg: 78, Mismatches: 0, Gaps: 0
US-09-867-753-2

ALIGNMENT 2
Query: 1 MARSLVHIVYGLSVQVQV.....IM-ANGELADPECVIVVD 184
Subject: 1 MARSLVHIVYGLSVQVQV.....IM-ANGELADPECVIVVD 184
Score: 986, Ident: 100.0, Pos: 184, Neg: 78, Mismatches: 0, Gaps: 0
US-09-867-753-2

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RESULT 2
US 09 764-864 1155
? Sequence 1155, Application US/09/74864
? Patent No. US2002014275A1
? GENERAL INFORMATION:
? TITLE OF INVENTION: Nucleic Acids, Proteins, and Antbodies
? FILE REFERENCE: P1223
? CURRENT APPLICATION NUMBER: us/09/74864
? PRIOR FILING DATE: 2001-01-17
? Prior application data removed consult FAIM or file wrapper
? NUMBER OF SEQ ID NOS: 1792
? SOFTWARE: Patent In Ver. 2.0
? SEQ ID NO 155
? LENGTH: 14
? TYPE: PRT
? ORGANISM: Homo sapiens
US 09 764-864 1155

Query Match 100.0% Score 986; DR 10; Length 194;
Best Local Similarity 100.0% Prod. No. 4c-78;
Matches 184; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MARSVDTVEVTSVYVVFISFEDLSAASAFHWGAGAGSMDNDNPPSPNHNEM 61
ID 11 MARSVDTVEVTSVYVVFISFEDLSAASAFHWGAGAGSMDNDNPPSPNHNEM 70
QY 61 MARSVDTVEVTSVYVVFISFEDLSAASAFHWGAGAGSMDNDNPPSPNHNEM 127
ID 71 MARSVDTVEVTSVYVVFISFEDLSAASAFHWGAGAGSMDNDNPPSPNHNEM 140
QY 121 MARSVDTVEVTSVYVVFISFEDLSAASAFHWGAGAGSMDNDNPPSPNHNEM 190
ID 131 MARSVDTVEVTSVYVVFISFEDLSAASAFHWGAGAGSMDNDNPPSPNHNEM 200
QY 181 IVDV 184
ID 191 IVDV 194
QY 191 IVDV 194
ID 191 IVDV 194

RESULT 4
US 09 764-864 1568
? Sequence 1568, Application US/09/74864
? Patent No. US2003005960A1
? GENERAL INFORMATION:
? TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
? FILE REFERENCE: P1223
? CURRENT APPLICATION NUMBER: US/09/764-864
? PRIOR FILING DATE: 2001-01-17
? Prior application data removed consult FAIM or file wrapper
? NUMBER OF SEQ ID NOS: 1792
? SOFTWARE: Patent In Ver. 2.0
? SEQ ID NO 1568
? LENGTH: 194
? TYPE: PRT
? ORGANISM: Homo sapiens
US 09 764-864 1568

Query Match 100.0% Score 972; DR 10; Length 194;
Best Local Similarity 97.1% Prod. No. 1-4c-78;
Matches 179; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 MARSVDTVEVTSVYVVFISFEDLSAASAFHWGAGAGSMDNDNPPSPNHNEM 60
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QY 61 MARSVDTVEVTSVYVVFISFEDLSAASAFHWGAGAGSMDNDNPPSPNHNEM 120
ID 71 MARSVDTVEVTSVYVVFISFEDLSAASAFHWGAGAGSMDNDNPPSPNHNEM 140
QY 121 MARSVDTVEVTSVYVVFISFEDLSAASAFHWGAGAGSMDNDNPPSPNHNEM 190
ID 131 MARSVDTVEVTSVYVVFISFEDLSAASAFHWGAGAGSMDNDNPPSPNHNEM 200
QY 181 IVDV 184
ID 191 IVDV 194
QY 191 IVDV 194
ID 191 IVDV 194

RESULT 5
US 10 158-160A-14
? Sequence 14, Application US/10/158160A
? Patent No. US2003005960A1
? GENERAL INFORMATION:
? TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
? FILE REFERENCE: P1223
? CURRENT APPLICATION NUMBER: US/10/158160A
? PRIOR FILING DATE: 2001-01-17
? Prior application data removed consult FAIM or file wrapper
? NUMBER OF SEQ ID NOS: 1792
? SOFTWARE: Patent In Ver. 2.0
? SEQ ID NO 1568
? LENGTH: 194
? TYPE: PRT
? ORGANISM: Homo sapiens
US 10 158-160A-14

Query Match 100.0% Score 178; DR 9; Length 194;
Best Local Similarity 45.2% Prod. No. 3-4c-08;
Matches 0; Conserved 14; Mismatches 24; Indels 0; Gaps 0;

QY 1 MARSVDTVEVTSVYVVFISFEDLSAASAFHWGAGAGSMDNDNPPSPNHNEM 152
ID 11 MARSVDTVEVTSVYVVFISFEDLSAASAFHWGAGAGSMDNDNPPSPNHNEM 160
QY 153 MARSVDTVEVTSVYVVFISFEDLSAASAFHWGAGAGSMDNDNPPSPNHNEM 165
ID 161 MARSVDTVEVTSVYVVFISFEDLSAASAFHWGAGAGSMDNDNPPSPNHNEM 170
QY 161 MARSVDTVEVTSVYVVFISFEDLSAASAFHWGAGAGSMDNDNPPSPNHNEM 173
ID 171 MARSVDTVEVTSVYVVFISFEDLSAASAFHWGAGAGSMDNDNPPSPNHNEM 180
QY 181 IVDV 184
ID 191 IVDV 194
QY 191 IVDV 194
ID 191 IVDV 194

RESULT 6
US 10 158-160A-14
? Sequence 14, Application US/10/158160A
? Patent No. US2003005960A1
? GENERAL INFORMATION:
? TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
? FILE REFERENCE: P1223
? CURRENT APPLICATION NUMBER: US/10/158160A
? PRIOR FILING DATE: 2001-01-17
? Prior application data removed consult FAIM or file wrapper
? NUMBER OF SEQ ID NOS: 1792
? SOFTWARE: Patent In Ver. 2.0
? SEQ ID NO 1568
? LENGTH: 194
? TYPE: PRT
? ORGANISM: Homo sapiens
US 10 158-160A-14

Query Match 100.0% Score 178; DR 9; Length 194;
Best Local Similarity 45.2% Prod. No. 3-4c-08;
Matches 0; Conserved 14; Mismatches 24; Indels 0; Gaps 0;

QY 1 MARSVDTVEVTSVYVVFISFEDLSAASAFHWGAGAGSMDNDNPPSPNHNEM 152
ID 11 MARSVDTVEVTSVYVVFISFEDLSAASAFHWGAGAGSMDNDNPPSPNHNEM 160
QY 153 MARSVDTVEVTSVYVVFISFEDLSAASAFHWGAGAGSMDNDNPPSPNHNEM 165
ID 161 MARSVDTVEVTSVYVVFISFEDLSAASAFHWGAGAGSMDNDNPPSPNHNEM 170
QY 161 MARSVDTVEVTSVYVVFISFEDLSAASAFHWGAGAGSMDNDNPPSPNHNEM 173
ID 171 MARSVDTVEVTSVYVVFISFEDLSAASAFHWGAGAGSMDNDNPPSPNHNEM 180
QY 181 IVDV 184
ID 191 IVDV 194
QY 191 IVDV 194
ID 191 IVDV 194

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Figure 7. Plot of $\ln \tau$ versus $\ln \tau_0$ for the Ti^{4+} and Zr^{4+} ions.

REFERENCES

79

RESULT 2
US 10-218 140-6224
GENERAL INFORMATION
APPLICANT: Leach, Martin D.
APPLICANT: Shinkets, Richard A.
TITLE OF INVENTION: N-VEL POLYNUCLEOTIDE
TITLE OF INVENTION: N-VEL POLYNUCLEOTIDE
FILE REFERENCE: 15966-543 CON


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QY 122 FURTHER INVESTIGATION: 19.78; Score 104.5; 100.0; Length 243;
Best Local Similarity: 29.08; Pred. No. 4, no 07;
Seq ID: 17; Conserved Loc: 27; Mismatches: 54; Indels: 0; Gaps: 0;

DB 114 FURTHER INVESTIGATION: 19.78; Score 104.5; 100.0; Length 243;
Best Local Similarity: 29.08; Pred. No. 4, no 07;
Seq ID: 17; Conserved Loc: 27; Mismatches: 54; Indels: 0; Gaps: 0;

RESULT 9
US 60/452,680 24132
Sequence 167, Application PC/TUS0247441
GENERAL INFORMATION:
APPLICANT: Berget, Allison
APPLICANT: Kambhampati, Subhadra
APPLICANT: Kambhampati, Subhadra
APPLICANT: Monahan, John E.
APPLICANT: Monahan, John E.
APPLICANT: Burdett, Lawrence J.
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: METHODS FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND
FILE REFERENCE: C0001450
CURRENT APPLICATION NUMBER: US 60/452,680
PRIORITY FILING DATE: 2002-04-05
PRIORITY FILING DATE: 2002-04-05
NUMBER OF SEQ ID NOS: 28
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 24132
LENGTH: 243
TYPE: PRT
ORGANISM: Homo Sapiens
US 60/452,680 24132

Query Match: 19.78; Score 104.5; 100.0; Length 243;
Best Local Similarity: 29.08; Pred. No. 4, no 07;
Matches: 49; Conserved Loc: 27; Mismatches: 54; Indels: 0; Gaps: 0;

QY 41 SEQUENCE 167, Application PC/TUS0247441
GENERAL INFORMATION:
APPLICANT: Berget, Allison
APPLICANT: Kambhampati, Subhadra
APPLICANT: Kambhampati, Subhadra
APPLICANT: Monahan, John E.
APPLICANT: Monahan, John E.
APPLICANT: Burdett, Lawrence J.
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: METHODS FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND
FILE REFERENCE: C0001450
CURRENT APPLICATION NUMBER: US 60/452,680
PRIORITY FILING DATE: 2002-04-05
PRIORITY FILING DATE: 2002-04-05
NUMBER OF SEQ ID NOS: 28
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 24132
LENGTH: 243
TYPE: PRT
ORGANISM: Homo Sapiens
US 60/452,680 24132

DB 114 FURTHER INVESTIGATION: 19.78; Score 104.5; 100.0; Length 243;
Best Local Similarity: 29.08; Pred. No. 4, no 07;
Seq ID: 17; Conserved Loc: 27; Mismatches: 54; Indels: 0; Gaps: 0;

QY 122 FURTHER INVESTIGATION: 19.78; Score 104.5; 100.0; Length 243;
Best Local Similarity: 29.08; Pred. No. 4, no 07;
Seq ID: 17; Conserved Loc: 27; Mismatches: 54; Indels: 0; Gaps: 0;

DB 114 FURTHER INVESTIGATION: 19.78; Score 104.5; 100.0; Length 243;
Best Local Similarity: 29.08; Pred. No. 4, no 07;
Seq ID: 17; Conserved Loc: 27; Mismatches: 54; Indels: 0; Gaps: 0;

RESULT 10
PCT-US02-37441-167
Sequence 167, Application PC/TUS0247441
GENERAL INFORMATION:
APPLICANT: Berget, Allison
APPLICANT: Kambhampati, Subhadra
APPLICANT: Kambhampati, Subhadra
APPLICANT: Monahan, John E.
APPLICANT: Monahan, John E.
APPLICANT: Burdett, Lawrence J.
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: METHODS FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND
FILE REFERENCE: C0001450
CURRENT APPLICATION NUMBER: US 60/452,680
PRIORITY FILING DATE: 2002-04-05
PRIORITY FILING DATE: 2002-04-05
NUMBER OF SEQ ID NOS: 28
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 167
LENGTH: 245
TYPE: PRT
ORGANISM: Homo Sapiens
US 10/401 922 167

Query Match: 19.78; Score 104.5; 100.0; Length 243;
Best Local Similarity: 29.08; Pred. No. 4, no 07;
Matches: 49; Conserved Loc: 27; Mismatches: 54; Indels: 0; Gaps: 0;

QY 122 FURTHER INVESTIGATION: 19.78; Score 104.5; 100.0; Length 243;
Best Local Similarity: 29.08; Pred. No. 4, no 07;
Seq ID: 17; Conserved Loc: 27; Mismatches: 54; Indels: 0; Gaps: 0;

DB 114 FURTHER INVESTIGATION: 19.78; Score 104.5; 100.0; Length 243;
Best Local Similarity: 29.08; Pred. No. 4, no 07;
Seq ID: 17; Conserved Loc: 27; Mismatches: 54; Indels: 0; Gaps: 0;

RESULT 12
US 60/452,680 24133
Sequence 24133, Application US/60452680
GENERAL INFORMATION:
APPLICANT: Cargill, Michele
APPLICANT: Cargill, Andrew

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ID	REL	NAME	DATE	TIME	LOCATION	FILE
164	REL	SECRET SERVICE	0001	0000000000		214
122	PROPERTY	TRAFLET	0001	0000000000	170	
215	PROPERTY	DAVIR	0001	0000000000	202	

Search completed: April 28, 2003, 05:12:24
Job time : 913 secs



Result	Score	Query	Length	IR	ID	Accession
1	206	20.9	341	1	SHX2_HUMAN	U06022 Homo sapiens
2	202	20.5	331	1	PXA_MOUSE	U06019 Mus musculus
3	202.5	20.5	331	1	SHX2_MOUSE	U06019 Mus musculus
4	191.5	19.4	371	1	CRY_MOUSE	U06049 Mus musculus
5	190.5	19.3	372	1	CRY_MOUSE	U06049 Mus musculus
6	189.5	19.2	369	1	ALX4_MOUSE	U06013 Mus musculus
7	188	19.1	402	1	P1X_MOUSE	U06013 Mus musculus
8	188	19.1	402	1	P1X_MOUSE	U06013 Mus musculus
9	187	19.0	366	1	CRY_MOUSE	U06049 Mus musculus
10	186.5	18.8	252	1	SHX2_HUMAN	U06022 Homo sapiens
11	184.5	18.7	372	1	CRY_MOUSE	U06049 Mus musculus
12	184.5	18.7	372	1	CRY_MOUSE	U06049 Mus musculus
13	184.5	18.7	245	1	P1X_MOUSE	U06013 Mus musculus
14	183	18.6	408	1	ALX4_MOUSE	U06013 Mus musculus
15	183	18.5	411	1	ALX4_MOUSE	U06013 Mus musculus
16	182.5	18.5	344	1	CRY_MOUSE	U06049 Mus musculus
17	182	18.5	247	1	SHX2_MOUSE	U06019 Mus musculus
18	182	18.5	240	1	ALX4_MOUSE	U06013 Mus musculus
19	182	18.5	336	1	PXA_MOUSE	U06019 Mus musculus
20	181.5	18.4	335	1	CRY_MOUSE	U06049 Mus musculus
21	181	18.4	413	1	CRY_MOUSE	U06049 Mus musculus
22	180	18.3	299	1	CRY_MOUSE	U06049 Mus musculus
23	180	18.3	299	1	CRY_MOUSE	U06049 Mus musculus
24	180	18.3	253	1	P1X_MOUSE	U06013 Mus musculus
25	179.5	18.2	337	1	P1X_MOUSE	U06013 Mus musculus
26	179	18.2	342	1	CRY_MOUSE	U06049 Mus musculus
27	179	18.2	873	1	CRY_MOUSE	U06049 Mus musculus
28	178.5	18.1	192	1	P1X_MOUSE	U06013 Mus musculus
29	178	18.1	240	1	CRY_MOUSE	U06049 Mus musculus
30	178	18.1	240	1	CRY_MOUSE	U06049 Mus musculus
31	178	18.1	563	1	PXA_MOUSE	U06019 Mus musculus
32	178	18.0	253	1	CRY_MOUSE	U06049 Mus musculus
33	177	18.0	253	1	CRY_MOUSE	U06049 Mus musculus
34	176.5	17.9	290	1	PXA_MOUSE	U06019 Mus musculus
35	176.5	17.9	290	1	PXA_MOUSE	U06019 Mus musculus

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Search completed. April 29, 2007, 21:14:05
Job time : 24 secs



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Search completed: April 28, 2003, 03:35:05
Job time : 74 secs

